

1/20 534 Rec'd PCT/PTC 14 JUL 2000

## SEQUENCE LISTING

&lt;110&gt; HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP

&lt;120&gt; HUMAN LYMPHOID PROTEIN TYROSINE PHOSPHATASES

&lt;130&gt; 3206-165

&lt;140&gt; PCT/CA99/00038

&lt;141&gt; 1999-01-18

&lt;160&gt; 6

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 3058

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (42)...(2465)

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 Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val Ala Glu Asn Ala Lys  
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 Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu Pro Tyr Asp Tyr Ser  
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cgg gta gaa cta tcc ctg ata acc tct gat gag gat tcc agc tac atc 296  
 Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu Asp Ser Ser Tyr Ile  
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Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala Cys Met Glu Tyr Glu			
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Met Gly Lys Lys Lys Cys Glu Arg Tyr Trp Ala Glu Pro Gly Glu Met			
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Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys Glu Ala Glu Lys Arg			
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aaa tct gat tat ata atc agg act cta aaa gtt aag ttc aat agt gaa		584	
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Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn Trp Pro Asp His Asp			
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Val Pro Ser Ser Ile Asp Pro Ile Leu Glu Leu Ile Trp Asp Val Arg			
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Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys Ile His Cys Ser Ala			
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Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile Val Asp Tyr Thr Trp			
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Met Leu Leu Lys Asp Gly Ile Ile Pro Glu Asn Phe Ser Val Phe Ser			
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Leu Ile Arg Glu Met Arg Thr Gln Arg Pro Ser Leu Val Gln Thr Gln			
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Lys His Cys Ile Pro Glu Lys Asn His Thr Leu Gln Ala Asp Ser Tyr			
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Gln Ala Gln Lys Val Met His Val Ser Ser Ala Glu Leu Asn Tyr Ser					
ctg cca tat gac tct aaa cac caa ata cgt aat gcc tct aat gta aag	505	510	515		1592
Leu Pro Tyr Asp Ser Lys His Gln Ile Arg Asn Ala Ser Asn Val Lys					
cac cat gac tct agt gct ctt ggt gta tat tct tac ata cct tta gtg	520	525	530		1640
His His Asp Ser Ser Ala Leu Gly Val Tyr Ser Tyr Ile Pro Leu Val					
gaa aat cct tat ttt tca tca tgg cct cca agt ggt acc agt tct aag	535	540	545		1688
Glu Asn Pro Tyr Phe Ser Ser Trp Pro Pro Ser Gly Thr Ser Ser Lys					
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Ser Leu Leu Pro Thr Ser Ser Thr Ser Leu Phe Ser Tyr Tyr Asn Ser					
cat agt tct tta tca ctg aat tct cca acc aat att tcc tca cta ttg	585	590	595		1832
His Ser Ser Leu Ser Leu Asn Ser Pro Thr Asn Ile Ser Ser Leu Leu					
aac cag gag tca gct gta cta gca act gct cca agg ata gat gat gaa	600	605	610		1880
Asn Gln Glu Ser Ala Val Leu Ala Thr Ala Pro Arg Ile Asp Asp Glu					
atc ccc cct cca ctt cct gta cgg aca cct gaa tca ttt att gtg gtt	615	620	625		1928
Ile Pro Pro Pro Leu Pro Val Arg Thr Pro Glu Ser Phe Ile Val Val					
gag gaa gct gga gaa ttc tca cca aat gtt ccc aaa tcc tta tcc tca	630	635	640	645	1976
Glu Glu Ala Gly Glu Phe Ser Pro Asn Val Pro Lys Ser Leu Ser Ser					
gct gtg aag gta aaa att gga aca tca ctg gaa tgg ggt gga aca tct	650	655	660		2024
Ala Val Lys Val Lys Ile Gly Thr Ser Leu Glu Trp Gly Gly Thr Ser					

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Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val  
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Ala Glu Asn Ala Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu  
50 55 60  
Pro Tyr Asp Tyr Ser Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu  
65 70 75 80  
Asp Ser Ser Tyr Ile Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro  
85 90 95  
Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp  
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130 135 140  
Glu Pro Gly Glu Met Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys  
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Glu Ala Glu Lys Arg Lys Ser Asp Tyr Ile Ile Arg Thr Leu Lys Val  
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Lys Phe Asn Ser Glu Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn  
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Trp Pro Asp His Asp Val Pro Ser Ser Ile Asp Pro Ile Leu Glu Leu  
195 200 205

Ile Trp Asp Val Arg Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys  
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Ile His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile  
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Val Asp Tyr Thr Trp Met Leu Leu Lys Asp Gly Ile Ile Pro Glu Asn  
245 250 255

Phe Ser Val Phe Ser Leu Ile Arg Glu Met Arg Thr Gln Arg Pro Ser  
260 265 270

Leu Val Gln Thr Gln Glu Gln Tyr Glu Leu Val Tyr Asn Ala Val Leu  
275 280 285

Glu Leu Phe Lys Arg Gln Met Asp Val Ile Arg Asp Lys His Ser Gly  
290 295 300

Thr Glu Ser Gln Ala Lys His Cys Ile Pro Glu Lys Asn His Thr Leu  
305 310 315 320

Gln Ala Asp Ser Tyr Ser Pro Asn Leu Pro Lys Ser Thr Thr Lys Ala  
325 330 335

Ala Lys Met Met Asn Gln Gln Arg Thr Lys Met Glu Ile Lys Glu Ser  
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Ser Ser Phe Asp Phe Arg Thr Ser Glu Ile Ser Ala Lys Glu Glu Leu  
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Val Leu His Pro Ala Lys Ser Ser Thr Ser Phe Asp Phe Leu Glu Leu  
370 375 380

Asn Tyr Ser Phe Asp Lys Asn Ala Asp Thr Thr Met Lys Trp Gln Thr  
385 390 395 400

Lys Ala Phe Pro Ile Val Gly Glu Pro Leu Gln Lys His Gln Ser Leu  
405 410 415

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Asp Leu Gly Ser Leu Leu Phe Glu Gly Cys Ser Asn Ser Lys Pro Val  
420 425 430

Asn Ala Ala Gly Arg Tyr Phe Asn Ser Lys Val Pro Ile Thr Arg Thr  
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Asp Ser Lys Glu Asn Phe Ser Tyr Leu Glu Ser Gln Pro His Asp Ser  
465 470 475 480

Cys Phe Val Glu Met Gln Ala Gln Lys Val Met His Val Ser Ser Ala  
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Glu Ile Asn Tyr Ser Leu Pro Tyr Asp Ser Lys His Gln Ile Arg Asn  
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Ala Ser Asn Val Lys His His Asp Ser Ser Ala Leu Gly Val Tyr Ser  
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Tyr Ile Pro Leu Val Glu Asn Pro Tyr Phe Ser Ser Trp Pro Pro Ser  
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Gly Thr Ser Ser Lys Met Ser Leu Asp Leu Pro Glu Lys Gln Asp Gly  
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580 585 590

Ile Ser Ser Leu Leu Asn Gln Glu Ser Ala Val Leu Ala Thr Ala Pro  
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Arg Ile Asp Asp Glu Ile Pro Pro Pro Leu Pro Val Arg Thr Pro Glu  
610 615 620

Ser Phe Ile Val Val Glu Glu Ala Gly Glu Phe Ser Pro Asn Val Pro  
625 630 635 640

Lys Ser Leu Ser Ser Ala Val Lys Val Lys Ile Gly Thr Ser Leu Glu  
645 650 655

Trp Gly Gly Thr Ser Glu Pro Lys Lys Phe Asp Asp Ser Val Ile Leu  
660 665 670

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Arg Pro Ser Lys Ser Val Lys Leu Arg Ser Pro Lys Ser Glu Leu His  
675 680 685

Gln Asp Arg Ser Ser Pro Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu  
690 695 700

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705 710 715 720

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725 730 735

Lys Gln Thr Leu Lys Thr Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser  
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755 760 765

Pro Asn Lys Pro Ala Glu Ser Val Gln Ser Asn Asn Ser Ser Ser Phe  
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Tyr	Lys	Ala	Asp	Lys	Thr	Tyr	Tyr	Pro	Thr	Thr	Val	Ala	Glu	Asn	Ala	Lys
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aat	atc	aag	aaa	aac	aga	tat	aag	gat	att	ttg	ccc	tat	gat	tat	agc	248
Asn	Ile	Lys	Lys	Asn	Arg	Tyr	Lys	Asp	Ile	Leu	Pro	Tyr	Asp	Tyr	Ser	
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cg	gta	gaa	cta	tcc	ctg	ata	acc	tct	gat	gag	gat	tcc	agc	tac	atc	296
Arg	Val	Glu	Leu	Ser	Leu	Ile	Thr	Ser	Asp	Glu	Asp	Ser	Ser	Tyr	Ile	
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aat	gcc	aac	ttc	att	aag	gga	gtt	tat	gga	ccc	aag	gct	tat	att	gcc	344
Asn	Ala	Asn	Phe	Ile	Lys	Gly	Val	Tyr	Gly	Pro	Lys	Ala	Tyr	Ile	Ala	
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acc	cag	gg	cct	tta	tct	aca	acc	ctc	ctg	gac	ttc	tgg	agg	atg	att	392
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tgg	gaa	tat	agt	gtc	ctt	atc	att	gtt	atg	gca	tgc	atg	gag	tat	gaa	440
Trp	Glu	Tyr	Ser	Val	Leu	Ile	Ile	Val	Met	Ala	Cys	Met	Glu	Tyr	Glu	
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Gln	Ieu	Glu	Phe	Gly	Pro	Phe	Ser	Val	Ser	Cys	Glu	Ala	Glu	Lys	Arg	
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Lys	Ser	Asp	Tyr	Ile	Ile	Arg	Thr	Leu	Lys	Val	Lys	Phe	Asn	Ser	Glu	
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Thr	Arg	Thr	Ile	Tyr	Gln	Phe	His	Tyr	Lys	Asn	Trp	Pro	Asp	His	Asp	
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gta	cct	tca	tct	ata	gac	cct	att	ctt	gag	ctc	atc	tgg	gat	gta	cgt	680
Val	Pro	Ser	Ser	Ile	Asp	Pro	Ile	Leu	Glu	Leu	Ile	Trp	Asp	Val	Arg	
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Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys Ile His Cys Ser Ala  
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 250 255 260

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 280 285 290

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 Gln Met Asp Val Ile Arg Asp Lys His Ser Gly Thr Glu Ser Gln Ala  
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 Lys Ser Ser Thr Ser Phe Asp Phe Leu Glu Leu Asn Tyr Ser Phe Asp  
 375 380 385

aaa aat gct gac aca acc atg aaa tgg cag aca aag gca ttt cca ata 1256  
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 390 395 400 405

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																480
																485
cag gct caa aaa gta atg cat gtt tct tca gca gaa ctg aat tat tca															1544	
Gln	Ala	Gln	Lys	Val	Met	His	Val	Ser	Ser	Ala	Glu	Leu	Asn	Tyr	Ser	
																490
																495
																500
ctg cca tat gac tct aaa cac caa ata cgt aat gcc tct aat gta aag															1592	
Leu	Pro	Tyr	Asp	Ser	Lys	His	Gln	Ile	Arg	Asn	Ala	Ser	Asn	Val	Lys	
																505
																510
																515
cac cat gac tct agt gct ctt ggt gta tat tct tac ata cct tta gtg															1640	
His	His	Asp	Ser	Ser	Ala	Leu	Gly	Val	Tyr	Ser	Tyr	Ile	Pro	Leu	Val	
																520
																525
																530
gaa aat cct tat ttt tca tca tgg cct cca agt ggt acc agt tct aag															1688	
Glu	Asn	Pro	Tyr	Phe	Ser	Ser	Trp	Pro	Pro	Ser	Gly	Thr	Ser	Ser	Lys	
																535
																540
																545
atg tct ctt gat tta cct gag aag caa gat gga act gtt ttt cct tct															1736	
Met	Ser	Leu	Asp	Leu	Pro	Glu	Lys	Gln	Asp	Gly	Thr	Val	Phe	Pro	Ser	
																550
																555
																560
																565
tct ctg ttg cca aca tcc tct aca tcc ctc ttc tct tat tac aat tca															1784	
Ser	Leu	Leu	Pro	Thr	Ser	Ser	Thr	Ser	Leu	Phe	Ser	Tyr	Tyr	Asn	Ser	
																570
																575
																580
cat agt tct tta tca ctg aat tct cca acc aat att tcc tca cta ttg															1832	
His	Ser	Ser	Leu	Ser	Leu	Asn	Ser	Pro	Thr	Asn	Ile	Ser	Ser	Leu	Leu	
																585
																590
																595
aac cag gag tca gct gta cta gca act gct cca agg ata gat gat gaa															1880	

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Asn	Gln	Glu	Ser	Ala	Val	Leu	Ala	Thr	Ala	Pro	Arg	Ile	Asp	Asp	Glu	
600							605									610
atc ccc cct cca ctt cct gta cgg aca cct gaa tca ttt att gtg gtt															1928	
Ile	Pro	Pro	Pro	Leu	Pro	Val	Arg	Thr	Pro	Glu	Ser	Phe	Ile	Val	Val	
615							620									625
gag gaa gct gga gaa ttc tca cca aat gtt ccc aaa tcc tta tcc tca															1976	
Glu	Glu	Ala	Gly	Glu	Phe	Ser	Pro	Asn	Val	Pro	Lys	Ser	Leu	Ser	Ser	
630							635				640					645
gct gtg aag gta aaa att gga aca tca ctg gaa tgg ggt gga aca tct															2024	
Ala	Val	Lys	Val	Lys	Ile	Gly	Thr	Ser	Leu	Glu	Trp	Gly	Gly	Thr	Ser	
650							655				660					
gaa cca aag aaa ttt gat gac tct gtg ata ctt aga cca agc aag agt															2072	
Glu	Pro	Lys	Lys	Phe	Asp	Asp	Ser	Val	Ile	Leu	Arg	Pro	Ser	Lys	Ser	
665							670				675					
gta aaa ctc cga agt cct aaa tca ggt aaa aat ttc tct tgg ctt															2117	
Val	Lys	Leu	Arg	Ser	Pro	Lys	Ser	Gly	Lys	Asn	Phe	Ser	Trp	Leu		
680							685				690					
tagatgacat ttagccctaa gattggaaga atggttcggt aagtttagag taattcactt															2177	
caggaagtta ctgggttccc ataatacgctt ccagtattca ttgatttatt tctggcttcc															2237	
ccagactaga aattttgtaa agagtcatgg gggaaagctag ggctaaccag aaaataaaaat															2297	
aaaaataatg ggataaaaaaa tcggaactac tggggccccc ctagtcggag cacatccgg															2356	
<210> 4																
<211> 692																
<212> PRT																
<213> Homo sapiens																
<400> 4																
Met	Asp	Gln	Arg	Glu	Ile	Leu	Gln	Lys	Phe	Leu	Asp	Glu	Ala	Gln	Ser	
1																15
Lys Lys Ile Thr Lys Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys																
20																30
Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val																
35																45
Ala Glu Asn Ala Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu																

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50 55 60

Pro Tyr Asp Tyr Ser Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu  
65 70 75 80

Asp Ser Ser Tyr Ile Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro  
85 90 95

Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp  
100 105 110

Phe Trp Arg Met Ile Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala  
115 120 125

Cys Met Glu Tyr Glu Met Gly Lys Lys Cys Glu Arg Tyr Trp Ala  
130 135 140

Glu Pro Gly Glu Met Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys  
145 150 155 160

Glu Ala Glu Lys Arg Lys Ser Asp Tyr Ile Ile Arg Thr Leu Lys Val  
165 170 175

Lys Phe Asn Ser Glu Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn  
180 185 190

Trp Pro Asp His Asp Val Pro Ser Ser Ile Asp Pro Ile Leu Glu Leu  
195 200 205

Ile Trp Asp Val Arg Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys  
210 215 220

Ile His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile  
225 230 235 240

Val Asp Tyr Thr Trp Met Leu Leu Lys Asp Gly Ile Ile Pro Glu Asn  
245 250 255

Phe Ser Val Phe Ser Leu Ile Arg Glu Met Arg Thr Gln Arg Pro Ser  
260 265 270

Leu Val Gln Thr Gln Glu Gln Tyr Glu Leu Val Tyr Asn Ala Val Leu  
275 280 285

Glu Leu Phe Lys Arg Gln Met Asp Val Ile Arg Asp Lys His Ser Gly  
290 295 300

Thr Glu Ser Gln Ala Lys His Cys Ile Pro Glu Lys Asn His Thr Leu

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305 310 315 320

Gln Ala Asp Ser Tyr Ser Pro Asn Leu Pro Lys Ser Thr Thr Lys Ala  
325 330 335Ala Lys Met Met Asn Gln Gln Arg Thr Lys Met Glu Ile Lys Glu Ser  
340 345 350Ser Ser Phe Asp Phe Arg Thr Ser Glu Ile Ser Ala Lys Glu Glu Leu  
355 360 365Val Leu His Pro Ala Lys Ser Ser Thr Ser Phe Asp Phe Leu Glu Leu  
370 375 380Asn Tyr Ser Phe Asp Lys Asn Ala Asp Thr Thr Met Lys Trp Gln Thr  
385 390 395 400Lys Ala Phe Pro Ile Val Gly Glu Pro Leu Gln Lys His Gln Ser Leu  
405 410 415Asp Leu Gly Ser Leu Leu Phe Glu Gly Cys Ser Asn Ser Lys Pro Val  
420 425 430Asn Ala Ala Gly Arg Tyr Phe Asn Ser Lys Val Pro Ile Thr Arg Thr  
435 440 445Lys Ser Thr Pro Phe Glu Leu Ile Gln Gln Arg Glu Thr Lys Glu Val  
450 455 460Asp Ser Lys Glu Asn Phe Ser Tyr Leu Glu Ser Gln Pro His Asp Ser  
465 470 475 480Cys Phe Val Glu Met Gln Ala Gln Lys Val Met His Val Ser Ser Ala  
485 490 495Glu Leu Asn Tyr Ser Leu Pro Tyr Asp Ser Lys His Gln Ile Arg Asn  
500 505 510Ala Ser Asn Val Lys His His Asp Ser Ser Ala Leu Gly Val Tyr Ser  
515 520 525Tyr Ile Pro Leu Val Glu Asn Pro Tyr Phe Ser Ser Trp Pro Pro Ser  
530 535 540Gly Thr Ser Ser Lys Met Ser Leu Asp Leu Pro Glu Lys Gln Asp Gly  
545 550 555 560

Thr Val Phe Pro Ser Ser Leu Leu Pro Thr Ser Ser Thr Ser Leu Phe

16/20

565

570

575

Ser Tyr Tyr Asn Ser His Ser Ser Leu Ser Leu Asn Ser Pro Thr Asn  
580 585 590

Ile Ser Ser Leu Leu Asn Gln Glu Ser Ala Val Leu Ala Thr Ala Pro  
595 600 605

Arg Ile Asp Asp Glu Ile Pro Pro Pro Leu Pro Val Arg Thr Pro Glu  
610 615 620

Ser Phe Ile Val Val Glu Glu Ala Gly Glu Phe Ser Pro Asn Val Pro  
625 630 635 640

Lys Ser Leu Ser Ser Ala Val Lys Val Lys Ile Gly Thr Ser Leu Glu  
645 650 655

Trp Gly Gly Thr Ser Glu Pro Lys Lys Phe Asp Asp Ser Val Ile Leu  
660 665 670

Arg Pro Ser Lys Ser Val Lys Leu Arg Ser Pro Lys Ser Gly Lys Asn  
675 680 685

Phe Ser Trp Leu  
690

<210> 5

<211> 802

<212> PRT

<213> Mus musculus

<400> 5

Met Asp Gln Arg Glu Ile Leu Gln Gln Leu Leu Lys Glu Ala Gln Lys  
1 5 10 15

Lys Lys Leu Asn Ser Glu Glu Phe Ala Ser Glu Phe Leu Lys Leu Lys  
20 25 30

Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Ile Tyr Pro Thr Thr Val  
35 40 45

Ala Gln Arg Pro Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu  
50 55 60

Pro Tyr Asp His Ser Leu Val Glu Leu Ser Leu Leu Thr Ser Asp Glu  
65 70 75 80

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Asp Ser Ser Tyr Ile Asn Ala Ser Phe Ile Lys Gly Val Tyr Gly Pro  
85 90 95

Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp  
100 105 110

Phe Trp Arg Met Ile Trp Glu Tyr Arg Ile Leu Val Ile Val Met Ala  
115 120 125

Cys Met Glu Phe Glu Met Gly Lys Lys Cys Glu Arg Tyr Trp Ala  
130 135 140

Glu Pro Gly Glu Thr Gln Leu Gln Phe Gly Pro Phe Ser Ile Ser Cys  
145 150 155 160

Glu Ala Glu Lys Lys Ser Asp Tyr Lys Ile Arg Thr Leu Lys Ala  
165 170 175

Lys Phe Asn Asn Glu Thr Arg Ile Ile Tyr Gln Phe His Tyr Lys Asn  
180 185 190

Trp Pro Asp His Asp Val Pro Ser Ser Ile Asp Pro Ile Leu Gln Leu  
195 200 205

Ile Trp Asp Met Arg Cys Tyr Gln Glu Asp Asp Cys Val Pro Ile Cys  
210 215 220

Ile His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Val  
225 230 235 240

Asp Tyr Thr Trp Met Leu Leu Lys Asp Gly Ile Ile Pro Lys Asn Phe  
245 250 255

Ser Val Phe Asn Leu Ile Gln Glu Met Arg Thr Gln Arg Pro Ser Leu  
260 265 270

Val Gln Thr Gln Glu Gln Tyr Glu Leu Val Tyr Ser Ala Val Leu Glu  
275 280 285

Leu Phe Lys Arg His Met Asp Val Ile Ser Asp Asn His Leu Gly Arg  
290 295 300

Glu Ile Gln Ala Gln Cys Ser Ile Pro Glu Gln Ser Leu Thr Val Glu  
305 310 315 320

Ala Asp Ser Cys Pro Leu Asp Leu Pro Lys Asn Ala Met Arg Asp Val  
325 330 335

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Lys Thr Thr Asn Gln His Ser Lys Gln Gly Ala Glu Ala Glu Ser Thr  
340 345 350

Gly Gly Ser Ser Leu Gly Leu Arg Thr Ser Thr Met Asn Ala Glu Glu  
355 360 365

Glu Leu Val Leu His Ser Ala Lys Ser Ser Pro Ser Phe Asn Cys Leu  
370 375 380

Glu Leu Asn Cys Gly Cys Asn Asn Lys Ala Val Ile Thr Arg Asn Gly  
385 390 395 400

Gln Ala Arg Ala Ser Pro Val Val Gly Glu Pro Leu Gln Lys Tyr Gln  
405 410 415

Ser Leu Asp Phe Gly Ser Met Leu Phe Gly Ser Cys Pro Ser Ala Leu  
420 425 430

Pro Ile Asn Thr Ala Asp Arg Tyr His Asn Ser Lys Gly Pro Val Lys  
435 440 445

Arg Thr Lys Ser Thr Pro Phe Glu Leu Ile Gln Gln Arg Lys Thr Asn  
450 455 460

Asp Ieu Ala Val Gly Asp Gly Phe Ser Cys Leu Glu Ser Gln Leu His  
465 470 475 480

Glu His Tyr Ser Leu Arg Glu Leu Gln Val Gln Arg Val Ala His Val  
485 490 495

Ser Ser Glu Glu Leu Asn Tyr Ser Leu Pro Gly Ala Cys Asp Ala Ser  
500 505 510

Cys Val Pro Arg His Ser Pro Gly Ala Leu Arg Val His Leu Tyr Thr  
515 520 525

Ser Leu Ala Glu Asp Pro Tyr Phe Ser Ser Ser Pro Pro Asn Ser Ala  
530 535 540

Asp Ser Lys Met Ser Phe Asp Leu Pro Glu Lys Gln Asp Gly Ala Thr  
545 550 555 560

Ser Pro Gly Ala Leu Leu Pro Ala Ser Ser Thr Thr Ser Phe Phe Tyr  
565 570 575

Ser Asn Pro His Asp Ser Leu Val Met Asn Thr Leu Thr Ser Phe Ser  
580 585 590

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Pro Pro Leu Asn Gln Glu Thr Ala Val Glu Ala Pro Ser Arg Arg Thr  
595 600 605

Asp Asp Glu Ile Pro Pro Leu Pro Glu Arg Thr Pro Glu Ser Phe  
610 615 620

Ile Val Val Glu Glu Ala Gly Glu Pro Ser Pro Arg Val Thr Glu Ser  
625 630 635 640

Leu Pro Leu Val Val Thr Phe Gly Ala Ser Pro Glu Cys Ser Gly Thr  
645 650 655

Ser Glu Met Lys Ser His Asp Ser Val Gly Phe Thr Pro Ser Lys Asn  
660 665 670

Val Lys Leu Arg Ser Pro Lys Ser Asp Arg His Gln Asp Gly Ser Pro  
675 680 685

Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu Ser Phe Phe Leu Ala Asp  
690 695 700

Glu Asp Cys Ile Gln Ala Gln Ala Val Gln Thr Ser Ser Thr Ser Tyr  
705 710 715 720

Pro Glu Thr Thr Glu Asn Ser Thr Ser Ser Lys Gln Thr Leu Arg Thr  
725 730 735

Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser Leu Lys Ile Phe Arg Asn  
740 745 750

Met Lys Lys Ser Val Cys Asn Ser Ser Ser Pro Ser Lys Pro Thr Glu  
755 760 765

Arg Val Gln Pro Lys Asn Ser Ser Ser Phe Leu Asn Phe Gly Phe Gly  
770 775 780

Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro Pro Ser Ala Trp  
785 790 795 800

Asn Met

<210> 6  
<211> 82  
<212> DNA  
<213> Homo sapiens

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<400> 6

aaactccgaa gtcctaaatc aggtaaaaat ttctcttggc ttt:gatgac atttagccct 60

aagattggaa gaatggttcg tt

82

<210> 7

<211> 14

<212> PRT

<213> *Homo sapiens*

<400> 7

Lys Leu Arg Ser Pro Lys Ser Gly Lys Asn Phe Ser Trp Leu

1

5

10